The bacteriocin arsenal of *Pseudomonas*

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Pseudomonas is a metabolically versatile genus that has acquired several antagonism-mediating mechanisms in order to gain ground in competitive niches. Besides antibiotics, *Pseudomonas* also secretes ribosomally encoded antibacterial proteins, designated bacteriocins. In *Pseudomonas aeruginosa*, large phage tail-like bacteriocins (R and F) and smaller modular bacteriocins (S pyocins) have previously been studied. More recently, M-type and L-type pyocins have been added to its antibacterial complement.

We performed a comprehensive analysis on available full and draft genomes of pseudomonads to explore their arsenal of bacteriocin genes. In addition to underlining the highly strain-specific nature of bacteriocinogeny, this genome mining revealed that the functional diversity of pseudomonad bacteriocins is much broader than estimated from the currently characterized bacteriocins. For S-type bacteriocins, the modular domain architecture apparently has driven extensive diversification. Toxin-immunity modules are combined with various target-specifying receptor-binding domains, suggesting that recombination events have taken place. In addition, these modules also appear in antagonism-mediating complexes of a different nature such as Rhs and CDI proteins. The dynamic nature of the pseudomonad bacteriocins is further illustrated by the occurrence of novel bacteriocin architectures in which two toxin modules are integrated, for example two DNase domains. In another group of bacteriocins, the L-type or lectin-like bacteriocins, a second functional type of antibacterial protein was identified. Contrary to classical L-type bacteriocins consisting of a lectin tandem, this novel subclass only hosts a single lectin domain, hence representing a novel type in which the strain-specific killing function is essentially condensed into a single lectin domain.